



SEQUENCE LISTING

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MCMAHON, ANDREW P.

<120> REGULATION OF LUNG TISSUE BY HEDGEHOG-LIKE POLYPEPTIDES,
AND FORMULATIONS AND USES RELATED THERETO

<130> HUV-032.01

<140> 09/394,020

<141> 1999-09-10

<150> 60/099,952

<151> 1998-09-11

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<170> PatentIn Ver. 2.1

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Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
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Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
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Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	
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Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
		115					120					125				
gat	gag	gac	ggt	cac	cat	ttt	gaa	gaa	tca	ctc	cac	tac	gag	gga	aga	432
Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
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Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr	
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Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
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Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	
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Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu	
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Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu	
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ttt	gtc	ctc	gac	aac	tca	acg	gaa	gat	ctc	cac	acc	atg	acc	gcc	gcg	864
Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala	
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Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	
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agc ggt cag ctt aaa tct gtc atc gtg cag cgg ata tac acg gag gag	960
Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	
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cag cgg ggc tcg ttc gca cca gtg act gca cat ggg acc att gtg gtc	1008
Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	
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gac aga ata ctg gcg tcc tgt tac gcc gta ata gag gac cag ggg ctt	1056
Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	
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gcg cat ttg gcc ttc gcg ccc gcc agg ctc tat tat tac gtg tca tca	1104
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	
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Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	
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Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	
385 390 395 400	
tgg ctt ttg gac agc aac atg ctt cat cct ttg ggg atg tca gta aac	1248
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Ser Ser	
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1 5 10 15	
ctg gta tgc tcg gga ctg gcg tgc gga ccg ggc agg ggg ttc ggg aag	96
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
20 25 30	

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Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
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ccc	aat	gtg	gcc	gag	aag	acc	cta	ggc	gcc	agc	gga	agg	tat	gaa	ggg	192
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	
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Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
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aac	ccc	gac	atc	ata	ttt	aag	gat	gaa	gaa	aac	acc	gga	gcg	gac	agg	288
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
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Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser	
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Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
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gac	gaa	gat	ggc	cac	cac	tca	gag	gag	tct	ctg	cac	tac	gag	ggc	cgc	432
Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
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gca	gtg	gac	atc	acc	acg	tct	gac	cgc	gac	cgc	agc	aag	tac	ggc	atg	480
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	Met	
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Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	
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Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
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Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu	
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Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val	
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Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	
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Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser	
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Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu	
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Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu	
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cgt	gac	ggg	gac	cgc	cgg	ctc	ctg	ccc	gcc	gct	gtg	cac	agc	gtg	acc	1008
Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr	
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Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly	
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acc	att	ctc	atc	aac	cgg	gtg	ctg	gcc	tcg	tgc	tac	gcg	gtc	atc	gag	1104
Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	
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Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His	
	370					375					380					
gcg	ctc	ctg	gct	gca	ctg	gcg	ccc	gcg	cgc	acg	gac	cgc	ggc	ggg	gac	1200
Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp	
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Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr	
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gct	cca	ggt	gct	gcc	gac	gct	ccg	ggt	gcg	ggg	gcc	acc	gcg	ggc	atc	1296
Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile	
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cac	tgg	tac	tcg	cag	ctg	ctc	tac	caa	ata	ggc	acc	tgg	ctc	ctg	gac	1344
His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp	
		435					440					445				
agc	gag	gcc	ctg	cac	ccg	ctg	ggc	atg	gcg	gtc	aag	tcc	agc	nnn	agc	1392
Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser	
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cgg	ggg	gcc	ggg	gga	ggg	gcg	cgg	gag	ggg	gcc						1425
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Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu	Leu	Leu		
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Leu	Leu	Val	Val	Pro	Ala	Ala	Trp	Gly	Cys	Gly	Pro	Gly	Arg	Val	Val		
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Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	Tyr	Lys		
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Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg		
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Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr		
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ccc	aat	tac	aat	cca	gac	atc	atc	ttc	aag	gac	gag	gag	aac	aca	ggc		344
Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly		
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Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	Ser	Leu		
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Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr		
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Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr		
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gag	ggc	cgc	gcg	gtg	gac	atc	acc	aca	tca	gac	cgc	gac	cgc	aat	aag		536
Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys		
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Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val		
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Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
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Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
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cgc	ctg	gag	agt	ggg	gcg	cgt	gtg	gcc	ttg	tca	gcc	gtg	agg	ccg	gga	728
Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
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Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
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Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	
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Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val	
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gct	ggg	gtg	cca	ggc	ctg	cag	cct	gcc	cgc	gtg	gca	gct	gtc	tct	aca	1016
Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr	
			310					315					320			
cac	gtg	gcc	ctc	ggg	gcc	tac	gcc	ccg	ctc	aca	aag	cat	ggg	aca	ctg	1064
His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu	
		325					330					335				
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Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His	
	340					345					350					
cac	ctg	gct	cag	ttg	gcc	ttc	tgg	ccc	ctg	aga	ctc	ttt	cac	agc	ttg	1160
His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu	
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gca	tgg	ggc	agc	tgg	acc	ccg	ggg	gag	ggg	gtg	cat	tgg	tac	ccc	cag	1208
Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln	
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ctg	ctc	tac	cgc	ctg	ggg	cgt	ctc	ctg	cta	gaa	gag	ggc	agc	ttc	cac	1256
Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His	
			390					395						400		

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Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

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1 5 10 15																	
gcg ctg cca gcc cag agc tgc ggg ccg ggc cgg ggg ccg gtt ggc cgg	96																
Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg																	
20 25 30																	
cgc cgc tat gcg cgc aag cag ctc gtg ccg cta ctc tac aag caa ttt	144																
Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe																	
35 40 45																	
gtg ccc ggc gtg cca gag cgg acc ctg ggc gcc agt ggg cca gcg gag	192																
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu																	
50 55 60																	
ggg agg gtg gca agg ggc tcc gag cgc ttc cgg gac ctc gtg ccc aac	240																
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn																	
65 70 75 80																	
tac aac ccc gac atc atc ttc aag gat gag gag aac agt gga gcc gac	288																
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp																	
85 90 95																	
cgc ctg atg acc gag cgt tgc aag gag agg gtg aac gct ttg gcc att	336																
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile																	
100 105 110																	
gcc gtg atg aac atg tgg ccc gga gtg cgc cta cga gtg act gag ggc	384																
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly																	
115 120 125																	

tgg gac gag gac ggc cac cac gct cag gat tca ctc cac tac gaa ggc	432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
130 135 140	
cgt gct ttg gac atc act acg tct gac cgc gac cgc aac aag tat ggg	480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
145 150 155 160	
ttg ctg gcg cgc ctc gca gtg gaa gcc ggc ttc gac tgg gtc tac tac	528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
gag tcc cgc aac cac gtc cac gtg tgc gtc aaa gct gat aac tca ctg	576
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
180 185 190	
gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg	624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
195 200 205	
tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gac tgg	672
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
210 215 220	
gtt ttg gcg gcc gat gcg tca ggc cgg gtg gtg ccc acg ccg gtg ctg	720
Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	
225 230 235 240	
ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg	768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	
245 250 255	
gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg	816
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
260 265 270	
gtg ttt gcc gct cga ggg ccg gcg ccc gcg cca ggc gac ttt gca ccg	864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
275 280 285	
gtg ttc gcg cgc cgg cta cgc gct ggg gac tgc gtg ctg gcg ccc ggc	912
Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
290 295 300	
ggg gat gcg ctt cgg cca gcg cgc gtg gcc cgt gtg gcg cgg gag gaa	960
Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
305 310 315 320	
gcc gtg ggc gtg ttc gcg ccg ctc acc gcg cac ggg acg ctg ctg gtg	1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
325 330 335	
aac gat gtc ctg gcc tct tgc tac gcg gtt ctg gag agt cac cag tgg	1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
340 345 350	

gcg cac cgc gct ttt gcc ccc ttg aga ctg ctg cac gcg cta ggg gcg 1104
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

ctg ctc ccc ggc ggg gcc gtc cag ccg act ggc atg cat tgg tac tct 1152
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

cgg ctc ctc tac cgc tta gcg gag gag cta ctg ggc tg 1190
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

<210> 9

<211> 1251

<212> DNA

<213> Brachydanio rerio

<220>

<221> CDS

<222> (1) .. (1248)

<400> 9

atg gac gta agg ctg cat ctg aag caa ttt gct tta ctg tgt ttt atc 48
 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

agc ttg ctt ctg acg cct tgt gga tta gcc tgt ggt cct ggt aga ggt 96
 Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
 20 25 30

tat gga aaa cga aga cac cca aag aaa tta acc ccg ttg gct tac aag 144
 Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

caa ttc atc ccc aac gtt gct gag aaa acg ctt gga gcc agc ggc aaa 192
 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
 50 55 60

tac gaa ggc aaa atc aca agg aat tca gag aga ttt aaa gag ctg att 240
 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
 65 70 75 80

ccg aat tat aat ccc gat atc atc ttt aag gac gag gaa aac aca aac 288
 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
 85 90 95

gct gac agg ctg atg acc aag cgc tgt aag gac aag tta aat tcg ttg 336
 Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
 100 105 110

gcc ata tcc gtc atg aac cac tgg ccc ggc gtg aaa ctg cgc gtc act 384
 Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

gaa ggc tgg gat gag gat ggt cac cat tta gaa gaa tct ttg cac tat 432
 Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
 130 135 140

gag gga cgg gca gtg gac atc act acc tca gac agg gat aaa agc aag	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
145 150 155 160	
tat ggg atg cta tcc agg ctt gca gtg gag gca gga ttc gac tgg gtc	528
Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
tat tat gaa tct aaa gcc cac ata cac tgc tct gtc aaa gca gaa aat	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
tca gtg gct gct aaa tca gga gga tgt ttt cct ggg tct ggg acg gtg	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	
195 200 205	
aca ctt ggt gat ggg acg agg aaa ccc atc aaa gat ctt aaa gtg ggc	672
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly	
210 215 220	
gac cgg gtt ttg gct gca gac gag aag gga aat gtc tta ata agc gac	720
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp	
225 230 235 240	
ttt att atg ttt ata gac cac gat ccg aca acg aga agg caa ttc atc	768
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile	
245 250 255	
gtc atc gag acg tca gaa cct ttc acc aag ctc acc ctc act gcc gcg	816
Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala	
260 265 270	
cac cta gtt ttc gtt gga aac tct tca gca gct tcg ggt ata aca gca	864
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala	
275 280 285	
aca ttt gcc agc aac gtg aag cct gga gat aca gtt tta gtg tgg gaa	912
Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu	
290 295 300	
gac aca tgc gag agc ctc aag agc gtt aca gtg aaa agg att tac act	960
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr	
305 310 315 320	
gag gag cac gag ggc tct ttt gcg cca gtc acc gcg cac gga acc ata	1008
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile	
325 330 335	
ata gtg gat cag gtg ttg gca tcg tgc tac gcg gtc att gag aac cac	1056
Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His	
340 345 350	
aaa tgg gca cat tgg gct ttt gcg ccg gtc agg ttg tgt cac aag ctg	1104
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu	
355 360 365	

atg acg tgg ctt ttt ccg gct cgt gaa tca aac gtc aat ttt cag gag 1152
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380

gat ggt atc cac tgg tac tca aat atg ctg ttt cac atc ggc tct tgg 1200
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400

ctg ctg gac aga gac tct ttc cat cca ctc ggg att tta cac tta agt 1248
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

tga 1251

<210> 10
 <211> 425
 <212> PRT
 <213> Gallus sp.

<400> 10
 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 1 5 10 15

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 20 25 30

Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
 85 90 95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
 100 105 110

Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
 145 150 155 160

Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
 195 200 205
 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
 225 230 235 240
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
 245 250 255
 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
 260 265 270
 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
 275 280 285
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
 290 295 300
 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 320
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
 325 330 335
 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
 340 345 350
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415
 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425

<210> 11
 <211> 396
 <212> PRT
 <213> Murine sp.

<400> 11
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160
 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175
 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190
 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205
 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220
 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255
 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300
 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 385 390 395

<210> 12
 <211> 411
 <212> PRT
 <213> Murine sp.

<400> 12
 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
 225 230 235 240
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
 245 250 255
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 13
 <211> 437
 <212> PRT
 <213> Murine sp.

<400> 13
 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30
 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45
 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60

Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	
65					70					75					80	
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	
				85					90					95		
Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
			100					105					110			
Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
		115					120					125				
Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
	130					135					140					
Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	
145					150					155					160	
Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
			165						170					175		
Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	
			180					185					190			
Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	
		195					200					205				
Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	
	210					215					220					
Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	
225					230					235					240	
Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	
			245						250					255		
Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	
		260						265					270			
Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	
		275					280					285				
Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	
	290					295					300					
Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	
305					310					315					320	
Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	
			325					330					335			
His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	
			340					345					350			
Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	
	355						360					365				

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
 370 375 380

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
 385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
 405 410 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
 420 425 430

Ala Val Lys Ser Ser
 435

<210> 14

<211> 418

<212> PRT

<213> Brachydanio rerio

<400> 14

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
 1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
 20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
 100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
 145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
 195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220

Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255

Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285

Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335

Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365

Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380

Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415

Ser Ser

<210> 15

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> Xaa at position 463 is any or unknown amino acid

<400> 15

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
 20 25 30
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60
 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80
 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95
 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
 100 105 110
 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125
 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140
 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
 145 150 155 160
 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175
 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190
 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
 195 200 205
 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
 210 215 220
 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
 225 230 235 240
 Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
 245 250 255
 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
 260 265 270
 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
 275 280 285
 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300
 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320

Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335
 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350
 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365
 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380
 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400
 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415
 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430
 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460
 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
 465 470 475

<210> 16
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15
 Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125
 Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140
 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175
 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205
 Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
 210 215 220
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
 225 230 235 240
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
 245 250 255
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
 325 330 335
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
 355 360 365
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
 370 375 380
 Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 17
 <211> 396
 <212> PRT
 <213> Homo sapiens

<400> 17

Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
1				5					10					15	
Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
			20					25					30		
Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
		35					40					45			
Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
	50					55					60				
Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
65					70					75					80
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
				85					90					95	
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
			100					105					110		
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
		115					120					125			
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
	130					135					140				
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
145					150					155					160
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
				165					170					175	
Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
			180					185					190		
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
		195					200					205			
Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210					215					220				
Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
225					230					235					240
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
				245					250					255	
Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
			260					265					270		

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

<210> 18

<211> 416

<212> PRT

<213> Brachydanio rerio

<400> 18

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
 145 150 155 160
 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175
 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190
 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205
 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240
 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255
 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270
 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285
 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300
 Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320
 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335
 Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350
 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

<210> 19

<211> 1416

<212> DNA

<213> Drosophila sp.

<220>

<221> CDS

<222> (1)..(1413)

<400> 19

atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc	48
Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr	
1 5 10 15	
tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag ttc cag	96
Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln	
20 25 30	
ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg	144
Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr	
35 40 45	
caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg	192
Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu	
50 55 60	
acc tct ctg gtg gcc ctg ctg ctg atc gtc ttg ccg atg gtc ttt agc	240
Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser	
65 70 75 80	
ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg	288
Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala	
85 90 95	
cgc aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc	336
Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser	
100 105 110	
gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg	384
Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg	
115 120 125	
gat tcg ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc	432
Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile	
130 135 140	
ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag	480
Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys	
145 150 155 160	
cgc tgc aag gag aag cta aac gtg ctg gcc tac tcg gtg atg aac gaa	528
Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu	
165 170 175	
tgg ccc ggc atc cgg ctg ctg gtc acc gag agc tgg gac gag gac tac	576
Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr	
180 185 190	
cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att	624
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile	
195 200 205	

gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg	672
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu	
210 215 220	
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac	720
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His	
225 230 235 240	
atc tac tgc tcc gtc aag tca gat tgc tgc atc agt tcc cac gtg cac	768
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His	
245 250 255	
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg	816
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg	
260 265 270	
aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc	864
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr	
275 280 285	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc	912
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg	
290 295 300	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga	960
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly	
305 310 315 320	
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg	1008
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro	
325 330 335	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag	1056
Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys	
340 345 350	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag	1104
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln	
355 360 365	
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg	1152
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro	
370 375 380	
ctg acc cgc gag ggc acc att gtg gtc aac tgc gtg gcc gcc agt tgc	1200
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys	
385 390 395 400	
tat gcg gtg atc aac agt cag tgc ctg gcc cac tgg gga ctg gct ccc	1248
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro	
405 410 415	
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag	1296
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln	
420 425 430	

ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc 1344
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
435 440 445

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atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg    1392
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
      450                455                460

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ccg cag agc tgg cgc cac gat tga 1416
Pro Gln Ser Trp Arg His Asp
465 470

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<210> 20
<211> 471
<212> PRT
<213> Drosophila sp.
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<400> 20
Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
      1              5              10              15
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Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
20 25 30

Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
35 40 45

Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
50 55 60

Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
65 70 75 80

Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
85 90 95

Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
100 105 110

Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
115 120 125

Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
130 135 140

Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
145 150 155 160

Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
165 170 175

Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
180 185 190

His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
195 200 205

Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
 210 215 220
 Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
 225 230 235 240
 Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
 245 250 255
 Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
 260 265 270
 Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
 275 280 285
 Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
 290 295 300
 Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
 305 310 315 320
 Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
 325 330 335
 Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
 340 345 350
 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
 355 360 365
 Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
 370 375 380
 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400
 Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415
 Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430
 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445
 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460
 Pro Gln Ser Trp Arg His Asp
 465 470

<210> 21

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate polypeptide sequence

<220>

<221> MOD_RES

<222> (7)

<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

<220>

<221> MOD_RES

<222> (9)

<223> Arg, His or Lys

<220>

<221> MOD_RES

<222> (44)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES

<222> (85)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES

<222> (93)

<223> Lys, Arg, His, Asn or Gln

<220>

<221> MOD_RES

<222> (98)

<223> Lys, Arg or His

<220>

<221> MOD_RES

<222> (112)

<223> Ser, Thr, Tyr, Trp or Phe

<220>

<221> MOD_RES

<222> (132)

<223> Lys, Arg or His

<220>

<221> MOD_RES

<222> (137)

<223> Met, Cys, Ser or Thr

<220>

<221> MOD_RES

<222> (139)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES

<222> (181)

<223> Leu, Val, Met, Thr or Ser

<220>
<221> MOD_RES
<222> (183)
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> (185)
<223> Gln, Asn, Glu, or Asp

<220>
<221> MOD_RES
<222> (186)
<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>
<221> MOD-RES
<222> (189)
<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>
<221> MOD_RES
<222> (191)
<223> Ala, Gly, Cys, Leu, Val or Met

<220>
<221> MOD_RES
<222> (196)
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>
<221> MOD_RES
<222> (200)
<223> Arg, Lys, Met or Ile

<220>
<221> MOD_RES
<222> (206)
<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>
<221> MOD_RES
<222> (207)
<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>
<221> MOD_RES
<222> (209)
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>
<221> MOD_RES
<222> (211)
<223> Leu, Val, Met or Ile

<220>
<221> MOD_RES
<222> (212)

<223> Phe, Tyr, Thr, His or Trp

<220>

<221> MOD_RES

<222> (216)

<223> Ile, Val, Leu or Met

<220>

<221> MOD_RES

<222> (217)

<223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>

<221> MOD_RES

<222> (219)

<223> Leu, Val, Met, Thr or Ser

<220>

<223> each Xaa may also be any amino acid.

<400> 21

Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Gly	Xaa	Arg	Arg	His	Pro	Lys	Lys	Leu
1				5					10					15	
Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
			20					25					30		
Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
		35					40					45			
Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
	50					55					60				
Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
65					70					75					80
Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
			85						90					95	
Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
			100					105					110		
Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
		115					120					125			
Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
	130					135					140				
Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
145					150					155					160
Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
				165					170					175	
Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
			180					185					190		

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
 195 200 205

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
 210 215 220

<210> 22

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate
 polypeptide sequence

<220>

<221> MOD_RES

<222> (7)

<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>

<221> MOD_RES

<222> (8)

<223> Gly, Ala, Val, Leu or Ile

<220>

<221> MOD_RES

<222> (9)

<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>

<221> MOD_RES

<222> (12)

<223> Lys, Arg or His

<220>

<221> MOD_RES

<222> (13)

<223> Phe, Trp, Tyr or an amino acid gap

<220>

<221> MOD_RES

<222> (14)

<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>

<221> MOD_RES

<222> (17)

<223> Asn, Gln, His, Arg or Lys

<220>

<221> MOD_RES

<222> (19)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES

<222> (22)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (27)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (29)
<223> Ser, Thr, Gln or Asn

<220>
<221> MOD_RES
<222> (30)
<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (31)
<223> Gly, Ala, Val, Leu, Ile or Pro

<220>
<221> MOD_RES
<222> (33)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (40)
<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>
<221> MOD_RES
<222> (41)
<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>
<221> MOD_RES
<222> (44)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (45)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (46)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (48)
<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>
<221> MOD_RES
<222> (53)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (54)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (71)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (79)
<223> Glu, Asp, Gln or Asn

<220>
<221> MOD_RES
<222> (83)
<223> Glu or Asp

<220>
<221> MOD_RES
<222> (84)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (85)
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> (87)
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> (95)
<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>
<221> MOD_RES
<222> (100)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (107)
<223> Trp, Phe, Tyr, Arg, His or Lys

<220>
<221> MOD_RES
<222> (114)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>

<221> MOD_RES

<222> (115)

<223> Gln, Asn, Asp or Glu

<220>

<221> MOD_RES

<222> (116)

<223> Asp or Glu

<220>

<221> MOD_RES

<222> (125)

<223> Gly, Ala, Val, Leu, or Ile

<220>

<221> MOD_RES

<222> (134)

<223> Arg, His or Lys

<220>

<221> MOD_RES

<222> (135)

<223> Asn, Gln, Thr or Ser

<220>

<221> MOD_RES

<222> (139)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>

<221> MOD_RES

<222> (141)

<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>

<221> MOD_RES

<222> (157)

<223> Arg, His or Lys

<220>

<221> MOD_RES

<222> (158)

<223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>

<221> MOD_RES

<222> (160)

<223> Gly, Ala, Val, Leu or Ile

<220>

<221> MOD_RES

<222> (162)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>

<221> MOD_RES
 <222> (166)
 <223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
 <221> MOD_RES
 <222> (167)
 <223> Asp or Glu

<220>
 <223> each Xaa may also be any amino acid.

<400> 22

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
 1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
 130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
 145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
 165

<210> 23
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(624)

<400> 23

atg tgg aaa tgg ata ctg aca cat tgt gcc tca gcc ttt ccc cac ctg	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
ccc ggc tgc tgc tgc tgc tgc ttt ttg ttg ctg ttc ttg gtg tct tcc	96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
gtc cct gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
gcc acc aac tct tct tcc tcc tcc ttc tcc tct cct tcc agc gcg gga	192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	
50 55 60	
agg cat gtg cgg agc tac aat cac ctt caa gga gat gtc cgc tgg aga	240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
aag cta ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg	288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
aag gtc agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag	336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc	384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	
aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa	432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	
130 135 140	
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga	480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	
145 150 155 160	
tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg	528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	
165 170 175	
tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca	576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	
180 185 190	
cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca	624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
195 200 205	
tag	627

<210> 24

<211> 208

<212> PRT

<213> Homo sapiens

<400> 24

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Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
 1           5           10           15

Pro Gly Cys Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser
      20           25           30

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
      35           40           45

Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
      50           55           60

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
      65           70           75           80

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
      85           90           95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
      100          105          110

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
      115          120          125

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
      130          135          140

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
      145          150          155          160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
      165          170          175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
      180          185          190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
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<210> 25

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

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gcgcgcttcg aagcgaggca gccagcgagg gagagagcga gcgggagcgc cggagcgagg 60
aaatcgatgc gcgc

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74

<210> 26
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 26
 gcgcgcagat ctgggaaagc gcaagagaga gcgcacacgc acacacccgc cgcgcgact 60
 cgggatccgc gcgc 74

<210> 27
 <211> 996
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: gene
 activation construct

<400> 27
 cgaagcgagg cagccagcga gggagagagc gagcgggcga gccggagcga ggaaatcgaa 60
 ggttcgaatc cttccccac caccatcact ttcaaaagtc cgaaagaatc tgctccctgc 120
 ttgtgtgttg gaggtcgctg agtagtgcg gcgtaaaatt taagctacaa caaggcaagg 180
 cttgaccgac aattgcatga agaactctgct taggggttagg cgttttgcgc tgcttcgcga 240
 tgtacggggc agatatacgc gttgacattg attattgact agttattaat agtaatcaat 300
 tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 360
 tggcccgctt ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 420
 tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact atttacggta 480
 aactgcccac ttggcagtac atcaagtgtg tcatatgcc agtacgcccc ctattgacgt 540
 caatgacggg aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 600
 tacttggcag tacatctacg tattagtcac cgctattacc atgggtgatgc ggttttggca 660
 gtacatcaat gggcgtggat agcggtttga ctacggggga tttccaagtc tccaccccat 720
 tgacgtcaat gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780
 caactccgcc ccattgacgc aaatgggcgg taggcgtgta cgggtggagg tctatataag 840
 cagagctctc tggctaacta gagaaccac tgcttactgg cttatcgaaa ttaatacgac 900
 tcactatagg gagaccaag cttggtaccg agctcggatc gatctgggaa agcgcaagag 960
 agagcgaca gcacacacc cgccgcgcgc actcgg 996

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense
construct

<400> 28
gtcctggcgc cgccgccgcc gtcgcc 26

<210> 29
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense
construct

<400> 29
ttccgatgac cggcctttcg cggtga 26

B!
Cmt
<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense
construct

<400> 30
gtgcacggaa aggtgcaggc cacact 26